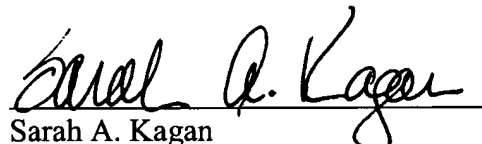## Remarks

New claims 59-85 are supported in the originally filed application. At paragraph 15, the specification teaches "that the genome of an organism can be sampled in groups of small pieces to determine karyotypic properties of an organism." At paragraph 21, the specification further teaches "enumeration of sequence tags generated is performed by determining the identity of the sequence tags and recording the number of occurrences of each such tag or of genomically clustered tags." At paragraph 22, the specification teaches: "A feature of the data analysis which enables the efficient practice of the method is the use of windows. These are groups of sequence tags which are genomically clustered.... Thus, for example, a window can comprise sequence tags that map within about 40kb, about 200 kb, about 600 kb, or about 4Mb." At paragraph 25, the specification teaches that tags are "matched to precise chromosomal locations, and tag densities are evaluated over moving windows to detect abnormalities in DNA sequence content." It is respectfully submitted that these portions, in particular, and the specification as a whole, fully support new claims 59-85.

Respectfully submitted,

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